

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=15; hr=15; min=12; sec=31; ms=949;]

=====

Application No:10719695

Version No:2.0

Input Set:

Output Set:

Started:2008-03-31 17:18:29.759

Finished:2008-03-31 17:18:30.007

Elapsed:0 hr(s) 0 min(s) 0 sec(s) 248 ms

Total Warnings:1

Total Errors:0

No. of SeqIDs Defined:3

Actual SeqID Count:3

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)

SEQUENCE LISTING

<110> NG, LEONG

<120> BODILY FLUID MARKERS OF TISSUE HYPOXIA

<130> ISA-012.01

<140> 10719695

<141> 2003-11-21

<150> GB 0322390.6

<151> 2003-09-24

<150> GB 0227179.9

<151> 2002-11-21

<160> 3

<170> PatentIn Ver. 3.2

<210> 1

<211> 999

<212> PRT

<213> Homo sapiens

<400> 1

Met	Ala	Asp	Lys	Val	Arg	Arg	Gln	Arg	Pro	Arg	Arg	Arg	Val	Cys	Trp
1				5					10					15	
Ala	Leu	Val	Ala	Val	Leu	Leu	Ala	Asp	Leu	Leu	Ala	Leu	Ser	Asp	Thr
			20					25					30		
Leu	Ala	Val	Met	Ser	Val	Asp	Leu	Gly	Ser	Glu	Ser	Met	Lys	Val	Ala
		35					40					45			
Ile	Val	Lys	Pro	Gly	Val	Pro	Met	Glu	Ile	Val	Leu	Asn	Lys	Glu	Ser
	50					55					60				
Arg	Arg	Lys	Thr	Pro	Val	Ile	Val	Thr	Leu	Lys	Glu	Asn	Glu	Arg	Phe
65					70					75					80
Phe	Gly	Asp	Ser	Ala	Ala	Ser	Met	Ala	Ile	Lys	Asn	Pro	Lys	Ala	Thr
			85						90					95	
Leu	Arg	Tyr	Phe	Gln	His	Leu	Leu	Gly	Lys	Gln	Ala	Asp	Asn	Pro	His
			100					105					110		
Val	Ala	Leu	Tyr	Gln	Ala	Arg	Phe	Pro	Glu	His	Glu	Leu	Thr	Phe	Asp
		115					120					125			
Pro	Gln	Arg	Gln	Thr	Val	His	Phe	Gln	Ile	Ser	Ser	Gln	Leu	Gln	Phe
	130					135					140				
Ser	Pro	Glu	Glu	Val	Leu	Gly	Met	Val	Leu	Asn	Tyr	Ser	Arg	Ser	Leu
145					150					155					160

Ala	Glu	Asp	Phe	Ala	Glu	Gln	Pro	Ile	Lys	Asp	Ala	Val	Ile	Thr	Val		
				165					170					175			
Pro	Val	Phe	Phe	Asn	Gln	Ala	Glu	Arg	Arg	Ala	Val	Leu	Gln	Ala	Ala		
				180				185					190				
Arg	Met	Ala	Gly	Leu	Lys	Val	Leu	Gln	Leu	Ile	Asn	Asp	Asn	Thr	Ala		
		195					200					205					
Thr	Ala	Leu	Ser	Tyr	Gly	Val	Phe	Arg	Arg	Lys	Asp	Ile	Asn	Thr	Thr		
	210					215					220						
Ala	Gln	Asn	Ile	Met	Phe	Tyr	Asp	Met	Gly	Ser	Gly	Ser	Thr	Val	Cys		
225					230				235						240		
Thr	Ile	Val	Thr	Tyr	Gln	Met	Val	Lys	Thr	Lys	Glu	Ala	Gly	Met	Gln		
				245				250						255			
Pro	Gln	Leu	Gln	Ile	Arg	Gly	Val	Gly	Phe	Asp	Arg	Thr	Leu	Gly	Gly		
			260					265					270				
Leu	Glu	Met	Glu	Leu	Arg	Leu	Arg	Glu	Arg	Leu	Ala	Gly	Leu	Phe	Asn		
		275					280					285					
Glu	Gln	Arg	Lys	Gly	Gln	Arg	Ala	Lys	Asp	Val	Arg	Glu	Asn	Pro	Arg		
	290					295					300						
Ala	Met	Ala	Lys	Leu	Leu	Arg	Glu	Ala	Asn	Arg	Leu	Lys	Thr	Val	Leu		
305					310				315						320		
Ser	Ala	Asn	Ala	Asp	His	Met	Ala	Gln	Ile	Glu	Gly	Leu	Met	Asp	Asp		
				325				330						335			
Val	Asp	Phe	Lys	Ala	Lys	Val	Thr	Arg	Val	Glu	Phe	Glu	Glu	Leu	Cys		
			340					345					350				
Ala	Asp	Leu	Phe	Glu	Arg	Val	Pro	Gly	Pro	Val	Gln	Gln	Ala	Leu	Gln		
		355					360					365					
Ser	Ala	Glu	Met	Ser	Leu	Asp	Glu	Ile	Glu	Gln	Val	Ile	Leu	Val	Gly		
	370					375					380						
Gly	Ala	Thr	Arg	Val	Pro	Arg	Val	Gln	Glu	Val	Leu	Leu	Lys	Ala	Val		
385					390				395						400		
Gly	Lys	Glu	Glu	Leu	Gly	Lys	Asn	Ile	Asn	Ala	Asp	Glu	Ala	Ala	Ala		
				405				410						415			
Met	Gly	Ala	Val	Tyr	Gln	Ala	Ala	Ala	Leu	Ser	Lys	Ala	Phe	Lys	Val		
			420					425					430				
Lys	Pro	Phe	Val	Val	Arg	Asp	Ala	Val	Val	Tyr	Pro	Ile	Leu	Val	Glu		
		435					440					445					
Phe	Thr	Arg	Glu	Val	Glu	Glu	Glu	Pro	Gly	Ile	His	Ser	Leu	Lys	His		
			450			455					460						

Asn	Lys	Arg	Val	Leu	Phe	Ser	Arg	Met	Gly	Pro	Tyr	Pro	Gln	Arg	Lys	
465					470					475					480	
Val	Ile	Thr	Phe	Asn	Arg	Tyr	Ser	His	Asp	Phe	Asn	Phe	His	Ile	Asn	
				485					490					495		
Tyr	Gly	Asp	Leu	Gly	Phe	Leu	Gly	Pro	Glu	Asp	Leu	Arg	Val	Phe	Gly	
			500					505					510			
Ser	Gln	Asn	Leu	Thr	Thr	Val	Lys	Leu	Lys	Gly	Val	Gly	Asp	Ser	Phe	
		515					520					525				
Lys	Lys	Tyr	Pro	Asp	Tyr	Glu	Ser	Lys	Gly	Ile	Lys	Ala	His	Phe	Asn	
	530					535					540					
Leu	Asp	Glu	Ser	Gly	Val	Leu	Ser	Leu	Asp	Arg	Val	Glu	Ser	Val	Phe	
545					550					555					560	
Glu	Thr	Leu	Val	Glu	Asp	Ser	Ala	Glu	Glu	Glu	Ser	Thr	Leu	Thr	Lys	
				565					570					575		
Leu	Gly	Asn	Thr	Ile	Ser	Ser	Leu	Phe	Gly	Gly	Gly	Thr	Thr	Pro	Asp	
			580					585						590		
Ala	Lys	Glu	Asn	Gly	Thr	Asp	Thr	Val	Gln	Glu	Glu	Glu	Glu	Ser	Pro	
		595					600					605				
Ala	Glu	Gly	Ser	Lys	Asp	Glu	Pro	Gly	Glu	Gln	Val	Glu	Leu	Lys	Glu	
	610					615					620					
Glu	Ala	Glu	Ala	Pro	Val	Glu	Asp	Gly	Ser	Gln	Pro	Pro	Pro	Pro	Glu	
625					630					635					640	
Pro	Lys	Gly	Asp	Ala	Thr	Pro	Glu	Gly	Glu	Lys	Ala	Thr	Glu	Lys	Glu	
				645					650					655		
Asn	Gly	Asp	Lys	Ser	Glu	Ala	Gln	Lys	Pro	Ser	Glu	Lys	Ala	Glu	Ala	
			660					665					670			
Gly	Pro	Glu	Gly	Val	Ala	Pro	Ala	Pro	Glu	Gly	Glu	Lys	Lys	Gln	Lys	
		675					680					685				
Pro	Ala	Arg	Lys	Arg	Arg	Met	Val	Glu	Glu	Ile	Gly	Val	Glu	Leu	Val	
	690					695					700					
Val	Leu	Asp	Leu	Pro	Asp	Leu	Pro	Glu	Asp	Lys	Leu	Ala	Gln	Ser	Val	
705					710					715					720	
Gln	Lys	Leu	Gln	Asp	Leu	Thr	Leu	Arg	Asp	Leu	Glu	Lys	Gln	Glu	Arg	
				725					730					735		
Glu	Lys	Ala	Ala	Asn	Ser	Leu	Glu	Ala	Phe	Ile	Phe	Glu	Thr	Gln	Asp	
			740					745					750			
Lys	Leu	Tyr	Gln	Pro	Glu	Tyr	Gln	Glu	Val	Ser	Thr	Glu	Glu	Gln	Arg	
		755					760						765			

Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp
770 775 780

Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu
785 790 795 800

Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys
805 810 815

Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Leu Asn His Ser
820 825 830

Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile
835 840 845

Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr
850 855 860

Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala
865 870 875 880

Thr Glu Lys Pro Val Leu Leu Ser Lys Asp Ile Glu Ala Lys Met Met
885 890 895

Ala Leu Asp Arg Glu Val Gln Tyr Leu Leu Asn Lys Ala Lys Phe Thr
900 905 910

Lys Pro Arg Pro Arg Pro Lys Asp Lys Asn Gly Thr Arg Ala Glu Pro
915 920 925

Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Glu Lys Val Ile Pro Pro
930 935 940

Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val
945 950 955 960

Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly
965 970 975

Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg
980 985 990

Pro Leu Lys Asn Asp Glu Leu
995

<210> 2
<211> 13
<212> PRT
<213> Homo sapiens

<400> 2
Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met
1 5 10

<210> 3

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 3

Cys	Leu	Ala	Val	Met	Ser	Val	Asp	Leu	Gly	Ser	Glu	Ser	Met
1				5					10				